

mRNA_SEQUENCE 1.0
 LOCUS AA639414 412 bp mRNA linear EST 23-OCT-1997
 DEFINITION ng89a12.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1159486 3',
 mRNA sequence.
 ACCESSION ~~AA639414~~
 VERSION AA639414.1 GI:2563193
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 412)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Ilian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40ml3 fwd. ET from Amersham.
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 /db_xref="taxon:9606"
 /clone="IMAGE:1159486"
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 /tissue_type="colon tumor RER+"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 RER+ colon tumor, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT7T3
 vector. Library is not normalized. Library was
 constructed by Bento Soares and M. Fatima Bonaldo (Soares4
)."
 BASE COUNT 84 a 129 c 117 g 82 t
 ORIGIN
 AA639414 Length: 412 May 23, 2003 18:23 Type: N Check: 7057 ..
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 51 AAACTAGAG GCCTTACATA GGCAGCTGG CCCAGCAGCT GGGTCCCTG
 101 ACCCAGGACT TCATTCTGGC CTGTCCCCC AAAGCATAGC CTCACCTTC
 151 TCACCTTCT CCAGAGGAGT CTCCTCCACC CCCACAGGAG CTGTGACAG
 201 GCCCTGCAGC CTTAGGGAAG GAGGAAGGT CCTGCAAGTA GACACTAAG
 251 CACAGCGCG CCCAGGGGTC ATAGGGCTC TTCTGGCGGT GGCATCTGCT
 301 GGGGCTTCCA GCTGGGCGAG GGCTCCACGC AACGGCTGAC CATCCAGAAG
 351 TAGTTGGGT GCACCTGGCC CTGCACGGCC TCGCTAACCA TCAATTCCCC
 401 ATCCACTGCA AA

Reverse
complement

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TOIG of reverse of aa639414 check: 7057 from: 1 to: 412
LOCUS      AA639414          412 bp  mRNA  linear  EST 23-OCT-1997
DEFINITION ng89a12.s1 NCI_CGAP_C09 Homo sapiens CDNA clone IMAGE:1159486 3'
ACCESSION  AA639414
VERSION    AA639414.1 GI:2563193
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 412)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL     Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.
            Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/dbp/image/image.html
            Seq primer: -40m13 fwd. RT from Amersham.
FEATURES
    source
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:1159486"
            /clone_id="NCI_CGAP_C09"
            /tissue_type="colon tumor RER+"
            /lab_host="DH10B"
            /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
            modified polylinker; 1st strand CDNA was prepared from
            RER+ colon tumor, and was then primed with a Not I -
            oligo(dT) primer. Double-stranded CDNA was ligated to Eco
            RI adaptors (Pharmacia), digested with Not I and cloned
            into the Not I and Eco RI sites of the modified pT7T3
            vector. Library is not normalized. Library was
            constructed by Bento Soares and M. Fatima Bonaldo (Soares4
            )".
    BASE COUNT      84 a      129 c      117 g      82 t
    ORIGIN
        AA639414 Length: 412 May 23, 2003 18:23 Type: N Check: 7057
        aa639414
        TTTGCAGTGGATGGGGAATTGATTAGCGAGCCGTCGACAGGGCCAGGTGCAACCAACTTCTTGA
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        ATGACCCCTGGGGCCGCGCTGTCCTTACTGTCAGGACCCCTTCCCTAGGGGCTGCAGG
        GCTGTGCACAGCTCTCTGTGGGGGTGAGGAGACTCTGTGGAGAGGGTGAGAGGTGAGGCTATGCT
        TTGGGGGAGACAGCCAGATGAGTCTGGGGTACGAGCCAGCTGCGGCCAGCTGCTATGTAAG
        GCCTTCTAGTTTGTGAGACCCCGCCACGACGAAATCCAAATTAAGTGACATTCCTCCT
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The list of best scores is:

1560 1570
AGCCTGAAAAAAAAAAAA

LOCUS A1042283 check: 5240 from: 1 to: 447
DEFINITION A1042283 447 bp mRNA linear EST 24-SEP-1998
OY13e09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens CDNA
clone IMAGE:165736 3', mRNA sequence.
ACCESSION A1042283
VERSION A1042283.1 GI:3281477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 447)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 693 Std Error: 0.00
Seq primer: -40ml3 fwd. EF from Amersham
High quality sequence stop: 376.
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:165736"
/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent_fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V-type: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot - 5. Library constructed by Bento
Soares and M.Fatima Bernaldo."
BASE COUNT 87 a 142 c 121 g 97 t
ORIGIN
; A1042283 Length: 447 May 23, 2003 18:21 Type: N Check: 5240 ..
a1042283
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TAAGGGCTCTTCTGGCGGTGGCATCTGTGGGGTCTCCAGCTGGCGGGGCTCCACGCAACCGCTGACC
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ACACACCTTCCCATCTGGGCTCA1

LOCUS AI042283 447 bp mRNA linear EST 24-SEP-1998
DEFINITION oyl3e09.xl Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
clone IMAGE:1665736 3', mRNA sequence.
ACCESSION AI042283
VERSION AI042283.1 GI:3281477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 693 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 376.
FEATURES
source
1. .447
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1665736"
/tissue_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: PT7T3D (Pharmacia) with a modified
polylinker V-TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTACCAATCTGAGTGGAGCGGCCGCAATTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified PT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 87 a 142 c 121 g 97 t
ORIGIN
AI042283 Length: 447 May 23, 2003 18:21 Type: N Check: 5240 ..
AI042283
TGGAGCCCAAGATGGAAAGTGTGTTGACATGATGGGGAATGATGTTAGCGAGCCGTGCAGGG
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CCTTCCCTTCTTCTGAGGCTGACAGGCTGTCCACAGCTCCTGGGGGTGAGAGACTCTCTGAG
AAGGTGAGAAGTGGAGGCTATGCTTGGGGGACAGGCTCAGATGAAGTCTGGGTACAGAGCCAGC
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AAATAAAGTGACATTCCTCCAAAAA1

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FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file us-09-937-060a-19.res made by shanley on wed 28 May 103 15:04:06-PDT.

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Query sequence being compared: US-09-937-060A-19 (1-1573)
Number of sequences searched: 1
Number of scores above cutoff: 1
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LOCUS       AI042283                447 bp    mRNA    linear    EST 24-SEP-1998
DEFINITION  oyl3e09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
ACCESSION   AI042283
VERSION     AI042283.1  GI:3281477
SOURCE      EST.
            human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1  (bases 1 to 447)
AUTHORS     NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncigap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
COMMENT     Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgaps-r@mail.nih.gov
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert length: 693 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 376.
FEATURES             Location/Qualifiers
     source          1..447
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="Soares_senescent_fibroblasts_NbHSF"
                     /tissue_type="senescent_fibroblast"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="vector: pT73D (Pharmacia) with a modified
                     polylinker V-type: phagemid; Site_1: Not I; Site_2: Eco RI
                     ; 1st strand cDNA was primed with a Not I - oligo(dT)
                     primer [5'
                     TCTTACCAATCTGAAGTGGGCGCGCCGCAATTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT73 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M. Fatima Bonaldo."
     BASE COUNT      87 a      142 c      121 g      97 t
     ORIGIN
a1042283  Length: 447 May 23, 2003 18:21 Type: N Check: 5240 ..
TTTTTTTGGGAATGTACTTTATTTGGATTGTGCTGCTGGGCTGGGGCTCAGAACAACTAGAGG
CCTTACATAGGCACCTGGGCCAGCCAGCTGGGCTCTGACAGCACTTCATTTCTGGCTGCCCA
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CCCTGCACCCCTTAGGGAAGAGAGGGTCTCTGCAAGTAGACATAAGGCACACGCGGCCAGGGTCA
TAAGGCTCTTCTGCGCGGTGCGACTCTGCGGCTTCAGCTGGGCGGGGCTCACGCAACCGGTGAC
ATCCAGAGATGATTGGTGCACCTGGCCACGCGCTCGCTAAGCAATTCATTCCTCCATCCACTGCA
ACACACCTTTCCATCTCTGGGCTCCAT

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> 0 <
0110 Intelligenetics
> 0 <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-937-060a-19.res made by shanley on Wed 28 May 103 15:04:06-PDT.

Query sequence being compared: US-09-937-060A-19 (1-1573)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-937-060A-19 (1-1573) with:
File: 42283rev.seq

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100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
E 5-
U -
E -
N -
C -
E -
S 0-----
SCORE 0 49 98 146 195 244 293 341 390 439
STDEV

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PARAMETERS

Similarity matrix	Unitary	K-tuple	4
Mismatch penalty	1	Joining penalty	30
Gap penalty	5.00	Window size	500
Gap size penalty	0.33		
Cutoff score	10		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	439	0	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

Number of residues:	447
Number of sequences searched:	1
Number of scores above cutoff:	1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Sig. Frame
1. a1042283	TOIG of reverse of: a1042283	447	439	442 0.00 0
1. US-09-937-060A-19 (1-1573)				
a1042283	TOIG of reverse of: a1042283	check: 5240	from: 1	
Initial Score = 439 Optimized Score = 442 Significance = 0.00				
Residue Identity = 98% Matches = 442 Mismatches = 5				
Gaps = 0 Conservative Substitutions = 0				
1100	1110	X 1120	1130	1140 1150 1160
GCCCGTGTGCGCTTCCGCTTGAGAGCCCAAGATGGAAGGCTTGTGACAGTGGGGAATGATGT				
TGAGCCCAAGATGGAAGGCTTGTGACAGTGGGGAATGATGT	X	10	20	30 40 50
1170	1180	1190	1200	1210 1220 1230
TAGCGAGGCGCGTGCAGGGCCAGGTGCACCAACTACTTCTGTGATGTCAGCGTTGCGTGGAGAGCCCGCC				
TAGCGAGGCGCGTGCAGGGCCAGGTGCACCAACTACTTCTGTGATGTCAGCGTTGCGTGGAGAGCCCGCC	60	70	80	90 100 110 120
1240	1250	1260	1270	1280 1290 1300 1310
CAGCTGGAAGCCCGACAGATGCGCCACCGCCAGAAAGCCCTTATGACCCCTGGCCGCGCTGTGCTTAGTG				
CAGCTGGAAGCCCGACAGATGCGCCACCGCCAGAAAGCCCTTATGACCCCTGGCCGCGCTGTGCTTAGTG	130	140	150	160 170 180 190
1320	1330	1340	1350	1360 1370 1380
TCTACTTGACAGACCTTCCCTCCCTCCCTAGGAGGCTGCGAGGCGCTGTCACAGCTCTGTGGGGTGAAGAG				
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1390	1400	1410	1420	1430 1440 1450
ACTCTCTGAGAGAAGGTGAGAAGGTGAGAGGCTATGCTTTGGGGGGACAGGCCCAATGAATGCTGGGTCA				
ACTCTCTGAGAGAAGGTGAGAAGGTGAGAGGCTATGCTTTGGGGGGACAGGCCCAATGAATGCTGGGTCA	270	280	290	300 310 320 330 340
1460	1470	1480	1490	1500 1510 1520
GGAGCCCAAGCTGGCTGGGGCCACAGCTGCTATGTAAGGCTTCTAGTTGTTCTGAGACCCCAAGCCCAAGAA				
GGAGCCCAAGCTGGCTGGGGCCACAGCTGCTATGTAAGGCTTCTAGTTGTTCTGAGACCCCAAGCCCAAGAA	350	360	370	380 390 400 410
1530	1540	1550	1560	1570
CCAAATCCAAATTAAGTGAATGACATTCACAGCCCTGAATAAAAAAAAAAAAAA				
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!!NA_SEQUENCE 1.0
LOCUS      AA639414                412 bp    mRNA    linear    EST 23-OCT-1997
DEFINITION ng89a12.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1159486 3',
            mRNA sequence.
ACCESSION  AA639414
VERSION    AA639414.1  GI:2563193
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 412)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
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            www-bio.llnl.gov/bdrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES
  source
    1. 412
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:1159486"
        /clone_1db="NCI_CGAP_Co9"
        /tissue_type="colon tumor RER+"
        /lab_host="DH10B"
        /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
        modified polylinker; 1st strand cDNA was prepared from
        RER+ colon tumor, and was then primed with a Not I -
        oligo(dT) primer. Double-stranded cDNA was ligated to Eco
        RI adaptors (Pharmacia), digested with Not I and cloned
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        )"
BASE COUNT  84 a . 129 c 117 g 82 t
ORIGIN
AA639414 Length: 412 May 23, 2003 18:23 Type: N Check: 7057 ..
1  GGAATGTCATTATTGCGATTGGTTCG TGGGGTGGGG GTCTCAGAAC
51  AAAC TAGAAG GCGTTACATA GGCAGCTGGG CCCAGCAGCT GGGTCCCTG
101  ACCCAGACT TCATTCTGGC CTGTCCCCC AAAGCATAGC CTCACCTTC
151  TCACCCCTCT CCAGAGAGT CTCTCCACC CCCACAGAG CTGTGACAG
201  GCCCTGCAGC CCTAGGGAAG GAGGAAGGT CCTGCAAGTA GACACTAAGG
251  CACAGCGCGG CCCAGGGGTC ATAGGGCTC TTCTGGCGGT GGCATCTGCT
301  GGGGCTTCCA GTGGGGCGAG GGTCCACGC AACCGCTGAC CATCCAGAAG
351  TAGTTGGGT GCACTGGCC CTGACGGCC TCGTAACCA TCATTTCCC
401  ATCCACTGCA AA

```

Reverse
complement

```
TOIG of Reverse of: aa639414 check: 7057 from: 1 to: 412
LOCUS      AA639414      412 bp      mRNA      linear      EST 23-OCT-1997
DEFINITION ng89a12.s1 NCI_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1159486 3',
ACCESSION  AA639414
VERSION    AA639414
KEYWORDS   AA639414.1 GI:2563193
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 412)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES   Location/Qualifiers
            source          1..412
                            /organism="Homo sapiens"
                            /db_xref="taxon:9606"
                            /clone="IMAGE:1159486"
                            /clone_lib="NCI_CGAP_Co9"
                            /tissue_type="colon tumor RER+"
                            /lab_host="DH10B"
                            /note="Organ: colon; Vector: pT7R3D-Pac (Pharmacia) with a
                            modified polylinker; 1st strand cDNA was prepared from
                            RER+ colon tumor, and was then primed with a Not I -
                            oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                            RI adaptors (Pharmacia), digested with Not I and cloned
                            into the Not I and Eco RI sites of the modified pT7R3
                            vector. Library is not normalized. Library was
                            constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                            )."
            BASE COUNT      84 a      129 c      117 g      82 t
            ORIGIN
            aa639414      Length: 412      May 23, 2003 18:23      Type: N      Check: 7057      ..
            TTTGAGTGGATGGGAATTGATGTTAGCGAGCCGTGACAGGGCCAGTGCACCCAACTACTTCTGGA
            TGGTCAGCGGTTGCGTGGAGCCCTGCGCCAGTGGAGCCCCAGATGCCACCGCAGAGAGCCCTT
            ATGACCCCTGGGCGCGCTGTGCTTAGTGTCTACTTGCAGAGCCCTTCTCTCTAGGGCTGCAGG
            GCCTGTCCACAGCTCCGTGGGGGTGAGAGACTCCCTGTGAGAGAGGAGAGAGTGAAGTGAAGCTATGCT
            TTGGGGGACAGGCCAGATGAATGATCTGTGGTCAAGGAGAACCCAGCTGTGGGCCCAAGCTGCTATGTAA
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